0047

Please replace paragraph [0066] on page 40 with the following paragraph.

0047

[0066] The deduced amino acid sequence from the OA/TAT cDNA sequence (Figure 1, SEQ ID NO:2) indicates an ORF of 670 amino acids constituting a protein of 74,645 Da molecular weight (DNA Star Software). Hydrophobicity analysis of the amino acid sequence suggests the presence of 12 potential transmembrane helices (~~www.isrec.isb-sib.ch/software/TMPRED_form.html~~). The lack of an identifiable signal sequence suggests that both NH_2- and -COOH terminals are located on the cytoplasmic face.

0048

Please replace paragraph [0067] beginning on page 40, and continuing onto page 41, with the following paragraph.

0048

[0067] The deduced amino acid sequence of OA/TAT shares up to 51% identity to the cloned mammalian monoamine transporters as determined by Clustal W-mp Multiple Sequence Alignment (~~http://www2.ebi.ac.uk/clustalw~~) described by Higgins et al. (1994) Nucleic Acids Res 22:4673. Among those that share the highest degree of identity with OA/TAT, are: mouse NET (50.4%), human DAT (49.8%), frog ET (49.5%) and mouse SERT (45.4%). The most conserved regions are the TM domains while the most variable ones are at the NH_3^+ terminal. The amino acid sequence also reveals possible function/regulation sites or motifs (~~www.motif.genome.ad.jp~~) as follows: a heptan leucine zipper motif (L-x(6)-L-x(6)-L-x(6)-L) present in the second TM (AA143 to AA164); two N-glycosylation sites (N-{P}-[ST]-{P}) on the second large extracellular loop (N240, N243) and phosphorylation sites for three different enzymes. The phosphorylation sites for protein kinase C (PKC)([ST]-x-[RK]) are: S39, T51, S59, S95 in the NH_2- terminal region, S308 between TM domain 4 and TM domain 5 and T635,

AMENDMENTS TO THE SPECIFICATION

0019
Please replace paragraph ~~[0021]~~ on page 9 with the following paragraph.

0019
~~[0021]~~ In another embodiment, the present invention provides isolated nucleic acids having at least about 60%, more preferably at least about 70%, at least about 75%, or at least about 80%, and most preferably at least about 90% or at least about 95%, sequence identity to the nucleic acid of SEQ ID NO: 1, wherein said nucleic acids encode a functional OA/TA transporter. Sequence identify is determined using the program Clustal W described by Higgins et al. (1994) Nucleic Acids Res. 22:4673 and may be calculated using the EMBL Nucleotide Sequence Database ~~(http://www.ebi.ac.uk/embl.html)~~.

0025
Please replace paragraph ~~[0044]~~ on page 24 with the following paragraph.

0025
~~[0044]~~ BLAST search ~~(http://www.nebi.nlm.nih.gov)~~ and amino acid sequence comparison (Lasergene, software package ~~or http://www2.ebi.ac.uk/clustalw/~~) were used to identify neurotransmitter transporter-like fragments from the PCR products amplified with degenerate primers or the PCR products obtained from nested RACE-PCR. BLAST was also used to determine the orientation and the position of the amplified products compared to the entire cDNA sequence.